

B/1



PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/913,728

DATE: 01/22/2002
TIME: 10:30:33

Input Set : A:\84335143.app
Output Set: N:\CRF3\01182002\I913728.raw

3 <110> APPLICANT: KITAMURA, TOSHI
4 FUJIO, KEISHI
6 <120> TITLE OF INVENTION: CYTOKINE RECEPTOR-LIKE PROTEINS
8 <130> FILE REFERENCE: 084335/0143
10 <140> CURRENT APPLICATION NUMBER: 09/913,728
C--> 11 <141> CURRENT FILING DATE: 2001-12-17
13 <150> PRIOR APPLICATION NUMBER: JP 1999-041936
14 <151> PRIOR FILING DATE: 1999-02-19
16 <160> NUMBER OF SEQ ID NOS: 34
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1278
22 <212> TYPE: DNA
23 <213> ORGANISM: Mus musculus
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (59)..(1135)
29 <400> SEQUENCE: 1

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32	atg gca tgg gca ctc gcg gtc atc ctc ctg cct cgg ctc ctt acg gcg	106
33	Met Ala Trp Ala Leu Ala Val Ile Leu Leu Pro Arg Leu Leu Thr Ala	
34	1 5 10 15	
36	gca gcg gcg gcg gcg gtg acg tca cgg ggt gat gtc aca gtc gtc	154
37	Ala Ala Ala Ala Ala Val Thr Ser Arg Gly Asp Val Thr Val Val	
38	20 25 30	
40	tgc cat gac ctg gag acg gtg gag gtc acg tgg ggc tcg ggc ccc gac	202
41	Cys His Asp Leu Glu Thr Val Glu Val Thr Trp Gly Ser Gly Pro Asp	
42	35 40 45	
44	cac cac ggc gcc aac ttg acg ctg gag ttc cgt tat ggt act ggc gcc	250
45	His His Gly Ala Asn Leu Ser Leu Glu Phe Arg Tyr Gly Thr Gly Ala	
46	50 55 60	
48	ctg caa ccc tgc ccg cga tat ttc ctg tcc ggc gct ggt gtc act tcc	298
49	Leu Gln Pro Cys Pro Arg Tyr Phe Leu Ser Gly Ala Gly Val Thr Ser	
50	65 70 75 80	
52	ggg tgc atc ctc ccc gcg agg gcg ggg ctg ctg gag ctg gca ctg	346
53	Gly Cys Ile Leu Pro Ala Ala Arg Ala Gly Leu Leu Glu Leu Ala Leu	
54	85 90 95	
56	cgc gac gga ggc ggg gcc atg gtg ttt aag gct agg cag cgc gcg tcc	394
57	Arg Asp Gly Gly Ala Met Val Phe Lys Ala Arg Gln Arg Ala Ser	
58	100 105 110	
60	gcc tgg ctg aag ccc cgc cca cct tgg aat gtg acg ctg ctc tgg aca	442
61	Ala Trp Leu Lys Pro Arg Pro Pro Trp Asn Val Thr Leu Leu Trp Thr	
62	115 120 125	

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64	cca	gac	ggg	gac	gtg	act	gtc	tcc	tgg	cct	gcc	cac	tcc	tac	ctg	ggc	490
65	Pro	Asp	Gly	Asp	Val	Thr	Val	Ser	Trp	Pro	Ala	His	Ser	Tyr	Leu	Gly	
66	130				135					140							
68	ctg	gac	tac	gag	gtg	cag	cac	cg	gag	agc	aat	gac	gat	gag	gac	gcc	538
69	Leu	Asp	Tyr	Glu	Val	Gln	His	Arg	Glu	Ser	Asn	Asp	Asp	Glu	Asp	Ala	
70	145				150				155		160						
72	tgg	cag	acg	acc	tca	ggg	ccc	tgc	tgt	gac	ttg	aca	gtg	ggc	ggg	ctc	586
73	Trp	Gln	Thr	Ser	Gly	Pro	Cys	Cys	Asp	Leu	Thr	Val	Gly	Gly	Leu		
74					165				170		175						
76	gac	ccc	gcg	cgc	tgc	tat	gac	ttc	cg	gtt	cg	g	cc	cg	gg	cc	634
77	Asp	Pro	Ala	Arg	Cys	Tyr	Asp	Phe	Arg	Val	Arg	Ala	Ser	Pro	Arg	Ala	
78					180				185		190						
80	gcy	cac	tat	ggc	ctg	gag	gcy	cag	cct	agc	gag	tgg	aca	gcy	gtg	aca	682
81	Ala	His	Tyr	Gly	Leu	Glu	Ala	Gln	Pro	Ser	Glu	Trp	Thr	Ala	Val	Thr	
82					195				200		205						
84	agg	ctt	tcc	ggg	gca	gca	tcc	gcy	gcc	tcc	tgt	acc	gca	agc	ccc	gcc	730
85	Arg	Leu	Ser	Gly	Ala	Ala	Ser	Ala	Ala	Ser	Cys	Thr	Ala	Ser	Pro	Ala	
86					210				215		220						
88	cca	tcc	ccg	gcc	ctg	gcc	ccg	ccc	ctc	ctg	ccc	ctg	ggc	tgc	ggc	cta	778
89	Pro	Ser	Pro	Ala	Leu	Ala	Pro	Pro	Leu	Leu	Pro	Leu	Gly	Cys	Gly	Leu	
90					225				230		235		240				
92	gca	gcy	ctg	ctg	aca	ctg	tcc	ctg	ctc	ctg	gcc	gcc	ctg	agg	ctt	cgc	826
93	Ala	Ala	Leu	Leu	Thr	Leu	Ser	Leu	Leu	Ala	Ala	Leu	Arg	Leu	Arg		
94					245				250		255						
96	agg	gtg	aaa	gat	gcy	ctg	ctg	ccc	tgc	gtc	cct	gac	ccc	agc	ggc	tcc	874
97	Arg	Val	Lys	Asp	Ala	Leu	Leu	Pro	Cys	Val	Pro	Asp	Pro	Ser	Gly	Ser	
98					260				265		270						
100	ttc	cct	gga	ctc	ttt	gag	aag	cat	cac	ggg	aac	ttc	cag	ggc	tgg	att	922
101	Phe	Pro	Gly	Leu	Phe	Glu	Lys	His	His	Gly	Asn	Phe	Gln	Ala	Trp	Ile	
102					275				280		285						
104	gcy	gac	gcc	cag	gcc	aca	gcc	ccg	cca	gcc	agg	acc	gag	gag	gaa	gat	970
105	Ala	Asp	Ala	Gln	Ala	Thr	Ala	Pro	Pro	Ala	Arg	Thr	Glu	Glu	Glu	Asp	
106					290				295		300						
108	gac	ctc	atc	cac	ccc	aag	gct	aag	agg	gtg	gag	ccc	gag	gac	ggc	acc	1018
109	Asp	Leu	Ile	His	Pro	Lys	Ala	Lys	Arg	Val	Glu	Pro	Glu	Asp	Gly	Thr	
110					305				310		315		320				
112	tcc	ctc	tgc	acc	gtg	cca	agg	cca	ccc	agc	tcc	gag	cca	agg	ggg	ccg	1066
113	Ser	Leu	Cys	Thr	Val	Pro	Arg	Pro	Pro	Ser	Phe	Glu	Pro	Arg	Gly	Pro	
114					325				330		335						
116	gga	ggc	ggg	gcc	atg	gtg	tca	gtg	ggc	ggg	gcc	acg	ttc	atg	gtg	ggc	1114
117	Gly	Gly	Gly	Ala	Met	Val	Ser	Val	Gly	Gly	Ala	Thr	Phe	Met	Val	Gly	
118					340				345		350						
120	gac	agc	ggc	tac	atg	acc	ctg	tgac	ttgaa	gtc	act	gcca	gtc	tata	actt		1165
121	Asp	Ser	Gly	Tyr	Met	Thr	Leu										
122					355												
124	caggctgagg	tcacttcctg	tctttaaata	attcaaactc	acaaatcc	tgc	ttg	atc	ttt	gtc	ttt	gtc	ttt	gtc	ttt	gtc	1225
126	tatgcaaatg	tgg	tac	gaa	tat	caa	ata	aa	atg	caa	at	gtat	gtc	aa	aaa		1278
129	<210>	SEQ ID NO:	2														
130	<211>	LENGTH:	359														

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131 <212> TYPE: PRT
132 <213> ORGANISM: Mus musculus
134 <400> SEQUENCE: 2
135 Met Ala Trp Ala Leu Ala Val Ile Leu Leu Pro Arg Leu Leu Thr Ala
136 1 5 10 15
138 Ala Ala Ala Ala Ala Val Thr Ser Arg Gly Asp Val Thr Val Val
139 20 25 30
141 Cys His Asp Leu Glu Thr Val Glu Val Thr Trp Gly Ser Gly Pro Asp
142 35 40 45
144 His His Gly Ala Asn Leu Ser Leu Glu Phe Arg Tyr Gly Thr Gly Ala
145 50 55 60
147 Leu Gln Pro Cys Pro Arg Tyr Phe Leu Ser Gly Ala Gly Val Thr Ser
148 65 70 75 80
150 Gly Cys Ile Leu Pro Ala Ala Arg Ala Gly Leu Leu Glu Leu Ala Leu
151 85 90 95
153 Arg Asp Gly Gly Gly Ala Met Val Phe Lys Ala Arg Gln Arg Ala Ser
154 100 105 110
156 Ala Trp Leu Lys Pro Arg Pro Pro Trp Asn Val Thr Leu Leu Trp Thr
157 115 120 125
159 Pro Asp Gly Asp Val Thr Val Ser Trp Pro Ala His Ser Tyr Leu Gly
160 130 135 140
162 Leu Asp Tyr Glu Val Gln His Arg Glu Ser Asn Asp Asp Glu Asp Ala
163 145 150 155 160
165 Trp Gln Thr Thr Ser Gly Pro Cys Cys Asp Leu Thr Val Gly Gly Leu
166 165 170 175
168 Asp Pro Ala Arg Cys Tyr Asp Phe Arg Val Arg Ala Ser Pro Arg Ala
169 180 185 190
171 Ala His Tyr Gly Leu Glu Ala Gln Pro Ser Glu Trp Thr Ala Val Thr
172 195 200 205
174 Arg Leu Ser Gly Ala Ala Ser Ala Ala Ser Cys Thr Ala Ser Pro Ala
175 210 215 220
177 Pro Ser Pro Ala Leu Ala Pro Pro Leu Leu Pro Leu Gly Cys Gly Leu
178 225 230 235 240
180 Ala Ala Leu Leu Thr Leu Ser Leu Leu Ala Ala Leu Arg Leu Arg
181 245 250 255
183 Arg Val Lys Asp Ala Leu Leu Pro Cys Val Pro Asp Pro Ser Gly Ser
184 260 265 270
186 Phe Pro Gly Leu Phe Glu Lys His His Gly Asn Phe Gln Ala Trp Ile
187 275 280 285
189 Ala Asp Ala Gln Ala Thr Ala Pro Pro Ala Arg Thr Glu Glu Glu Asp
190 290 295 300
192 Asp Leu Ile His Pro Lys Ala Lys Arg Val Glu Pro Glu Asp Gly Thr
193 305 310 315 320
195 Ser Leu Cys Thr Val Pro Arg Pro Pro Ser Phe Glu Pro Arg Gly Pro
196 325 330 335
198 Gly Gly Gly Ala Met Val Ser Val Gly Gly Ala Thr Phe Met Val Gly
199 340 345 350
201 Asp Ser Gly Tyr Met Thr Leu
202 355

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Input Set : A:\84335143.app

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205 <210> SEQ ID NO: 3
 206 <211> LENGTH: 804
 207 <212> TYPE: DNA
 208 <213> ORGANISM: Mus musculus
 210 <220> FEATURE:
 211 <221> NAME/KEY: CDS
 212 <222> LOCATION: (98)..(661)
 214 <400> SEQUENCE: 3

215 cqttttcgcc tctaagcgcc ctgggcgcgg tcgactcgga ccggctcgga ccgaaccaggc 60
 217 tqtcaatcac tgcagcggtcc gggggccccc cggcgac atg gca tgg gca ctc gcg 115
 218 Met Ala Trp Ala Leu Ala
 219 1 5
 221 gtc atc ctc ctg cct cgg ctc ctt acg gcg gca gcg gcg gcg gcg 163
 222 Val Ile Leu Leu Pro Arg Leu Leu Thr Ala Ala Ala Ala Ala Ala
 223 10 15 20
 225 gtg acg tca cgg ggt gat gtc aca gtc gtc tgc cat gac ctg gag acg 211
 226 Val Thr Ser Arg Gly Asp Val Thr Val Val Cys His Asp Leu Glu Thr
 227 25 30 35
 229 gtg gag gtc acg tgg ggc tcg ggc ccc gac cac cac ggc gcc aac ttg 259
 230 Val Glu Val Thr Trp Gly Ser Gly Pro Asp His His Gly Ala Asn Leu
 231 40 45 50
 233 agc ctg gag ttc cgt tat ggt act ggc gcc ctg caa ccc tgc ccg cga 307
 234 Ser Leu Glu Phe Arg Tyr Gly Thr Gly Ala Leu Gln Pro Cys Pro Arg
 235 55 60 65 70
 237 tat ttc ctg tcc ggc gct ggt gtc act tcc ggg tgc atc ctc ccc gcg 355
 238 Tyr Phe Leu Ser Gly Ala Gly Val Thr Ser Gly Cys Ile Leu Pro Ala
 239 75 80 85
 241 gcg agg gcg ggg ctg ctg gag ctg gca ctg cgc gac gga ggc ggg gcc 403
 242 Ala Arg Ala Gly Leu Leu Glu Leu Ala Leu Arg Asp Gly Gly Ala
 243 90 95 100
 245 atg gtg ttt aag gct agg cag cgc gcg tcc gcc tgg ctg aag ccc cgc 451
 246 Met Val Phe Lys Ala Arg Gln Arg Ala Ser Ala Trp Leu Lys Pro Arg
 247 105 110 115
 249 cca cct tgg aat gtg acg ctg ctc tgg aca cca gac ggg gac gtg act 499
 250 Pro Pro Trp Asn Val Thr Leu Leu Trp Thr Pro Asp Gly Asp Val Thr
 251 120 125 130
 253 gtc tcc tgg cct gcc cac tcc tac ctg ggc ctg gac tac gag gtg cag 547
 254 Val Ser Trp Pro Ala His Ser Tyr Leu Gly Leu Asp Tyr Glu Val Gln
 255 135 140 145 150
 257 cac cgg gag agc aat gac gat gag gac gcc tgg cag acg acc tca ggg 595
 258 His Arg Glu Ser Asn Asp Asp Glu Asp Ala Trp Gln Thr Ser Gly
 259 155 160 165
 261 ccc tgc tgt gac ttg aca gtg ggc ggg gcc acg ttc atg gtg ggc gac 643
 262 Pro Cys Cys Asp Leu Thr Val Gly Ala Thr Phe Met Val Gly Asp
 263 170 175 180
 265 agc ggc tac atg acc ctg tgaccttgaa gtcactgcc a tctatactt 691
 266 Ser Gly Tyr Met Thr Leu
 267 185
 269 caggctgagg tcacttcctg tctttaaata attcaaactc acaaatcctg tgcctgtctg 751

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271 tatgcaaatg tggcacgaa tattcaaata aatgcaaat gctatgctaa aaa 804
 274 <210> SEQ ID NO: 4
 275 <211> LENGTH: 188
 276 <212> TYPE: PRT
 277 <213> ORGANISM: Mus musculus
 279 <400> SEQUENCE: 4
 280 Met Ala Trp Ala Leu Ala Val Ile Leu Leu Pro Arg Leu Leu Thr Ala
 281 1 5 10 15
 283 Ala Ala Ala Ala Ala Val Thr Ser Arg Gly Asp Val Thr Val Val
 284 20 25 30
 286 Cys His Asp Leu Glu Thr Val Glu Val Thr Trp Gly Ser Gly Pro Asp
 287 35 40 45
 289 His His Gly Ala Asn Leu Ser Leu Glu Phe Arg Tyr Gly Thr Gly Ala
 290 50 55 60
 292 Leu Gln Pro Cys Pro Arg Tyr Phe Leu Ser Gly Ala Gly Val Thr Ser
 293 65 70 75 80
 295 Gly Cys Ile Leu Pro Ala Ala Arg Ala Gly Leu Leu Glu Leu Ala Leu
 296 85 90 95
 298 Arg Asp Gly Gly Ala Met Val Phe Lys Ala Arg Gln Arg Ala Ser
 299 100 105 110
 301 Ala Trp Leu Lys Pro Arg Pro Pro Trp Asn Val Thr Leu Leu Trp Thr
 302 115 120 125
 304 Pro Asp Gly Asp Val Thr Val Ser Trp Pro Ala His Ser Tyr Leu Gly
 305 130 135 140
 307 Leu Asp Tyr Glu Val Gln His Arg Glu Ser Asn Asp Asp Glu Asp Ala
 308 145 150 155 160
 310 Trp Gln Thr Thr Ser Gly Pro Cys Cys Asp Leu Thr Val Gly Gly Ala
 311 165 170 175
 313 Thr Phe Met Val Gly Asp Ser Gly Tyr Met Thr Leu
 314 180 185
 317 <210> SEQ ID NO: 5
 318 <211> LENGTH: 19
 319 <212> TYPE: DNA
 320 <213> ORGANISM: Artificial Sequence
 322 <220> FEATURE:
 323 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 325 <400> SEQUENCE: 5
 326 ggggggtggac catccctcta 19
 329 <210> SEQ ID NO: 6
 330 <211> LENGTH: 20
 331 <212> TYPE: DNA
 332 <213> ORGANISM: Artificial Sequence
 334 <220> FEATURE:
 335 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 337 <400> SEQUENCE: 6
 338 cqcgcaagctg taaacggtag 20
 341 <210> SEQ ID NO: 7
 342 <211> LENGTH: 25
 343 <212> TYPE: DNA



VERIFICATION SUMMARY
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L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:674 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:677 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:753 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34